In the Specification:

Please amend the specification as shown:

Please delete the paragraph on page 25, lines 16-29 and replace it with the following paragraph:

--Of the genes that increased in expression from 48h to 123h, 10 were in the tolerant cultures with increases ranging from 1.71 fold to 4.00 fold. Expression of the same genes in the rejection response showed either no increase in expression or a decrease in expression (Table 1(a)). Of particular note was axotrophin, a newly discovered stem cell gene; cyclin B2, associated with the cell cycle and cellular migration; histone H2A-X that may play a role in chromatin remodeling; and ELKL **(SEQ ID NO: 5)** motif kinase, also known as Erk, required to regulate the immune response and protect against auto-immunity. Table 1(b) shows the 5 genes that increased in expression in rejection. Again this increase was specific to rejection, with the exception of granzyme B with a twofold increase in both tolerance and rejection; however, the actual levels of granzyme B mRNA were six times greater in rejection than in tolerance. The 12-fold increase in Interferon gamma mRNA in rejection was in accord with our previous findings of high Interferon gamma protein release in these cultures.--

Please delete the paragraph on page 25, line 31 to page 26, line 5 and replace it with the following paragraph:

--Of those genes that showed high expression at 123h, within the context of the four arrays, 15 were in the tolerant set (Table 2(a)) and included axotrophin. In rejection, 13 genes are ranked in order of expression level in Table 2(b) with granzyme B and Interferon gamma being the highest. This analytical approach therefore showed correlation with phenotype with respect to granzyme B and Interferon gamma, and again placed axotrophin as being associated with tolerance, although the actual expression level was not great. A further analysis was made, identifying those genes that showed increased expression in tolerance whilst

showing a decreased expression in rejection (Table 3). This revealed Histone H2A-X, involved in chromatin structure and remodeling ; ELKL **(SEQ ID NO: 5)** motif kinase ; splicing factor 3b subunit 1 (SF3b-155), acting as part of the mRNA splicing complex and probably involved in exon removal; and cyclin B2, a regulator of the cell cycle and also involved in cellular migration when complexed with cdc2.--

Please delete Table 1a and 1b and replace it with the following table:

Table 1a and 1b: Genes showing increased expression (48h *versus* 123h)

Gene	Accession Number	Tolerance: Fold increase	*Rejection: Fold increase*
TOLERANCE			
Dual specificity phosphatase 1	X61940	**4.00**	*0.99*
BCL2-like 11	AA796690	**3.11**	*1.15*
*Axotrophin**	AW212859	**2.9**	*1.00*
H2A histone family, member X	M33988	**2.22**	*0.46*
Interferon stimulated protein (20kDa)	AW122677	**2.21**	*0.95*
Chemokine (C-C) receptor 6	AJ222714	**2.02**	*0.95*
Cyclin B2	X66032	**2.01**	*0.59*
Paneth cell enhanced expression	U37351	**2.0**	*0.98*
Splicing factor 3b, sub-unit 1, 155kDa	A1844532	**1.93**	*0.59*
*ELKL **(SEQ ID NO: 5)** motif kinase***	X70764	**1.71**	*0.63*
REJECTION			
Interferon gamma	K00083	0.69	***11.98***
Glutaryl CoA dehydrogenase	U18992	1.20	***5.10***
CD3 antigen, gamma polypeptide	M18228	1.23	***3.22***
Interleukin 1 receptor antagonist	L32838	1.00	***2.57***
Granzyme B	M12302	2.07	***2.52***

Please delete Table 3 and replace it with the following table:

Table 3. Genes showing increases in expression in tolerance *and* decreased expression in rejection

Gene	**Accession Number**	**Gene description**
H2A histone family, member X	M33988	Chromatin remodeling (Bassing; Bruno)
ELKL ***(SEQ ID NO: 5)*** *motif kinase***	X70764	Immune regulation ((Hurov)
Splicing factor 3b, subunit 1, 155kDa	A1844532	RNA splicing, intron removal (Horie)
Cyclin B2	X66032	Cell cycle; cell migration (Manes)